

Fig. 1 Junghans

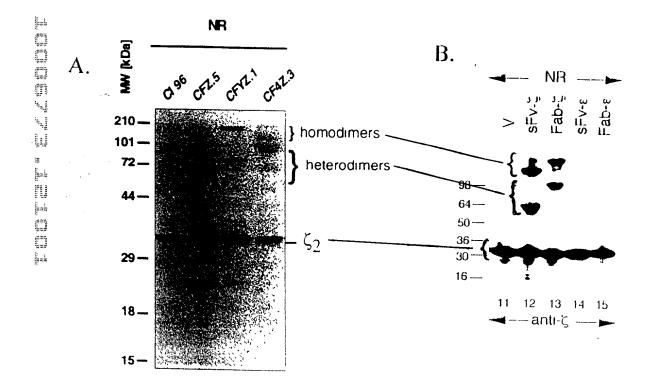


Fig. 2 Junghous

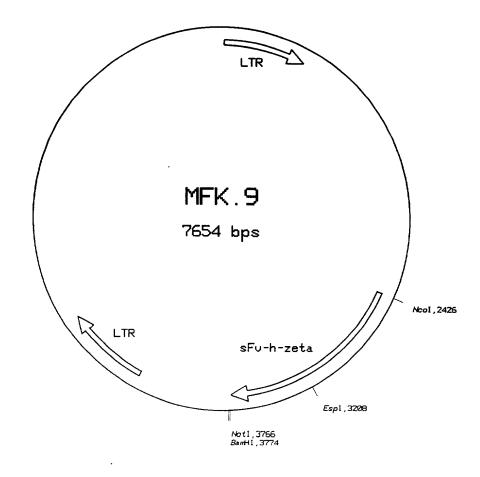


Fig. 3 Linghans

NAME: BMB3.6-H-Ch 504 BPS DNA UPDATED 6/25/93

DESCRIPTION: Heavy chain leader and variable region of BMB3.6-h

* * * * SEQUENCE * * *

1	TCACCATGAA	CTTCGGGTTC	AGCTTGATTT	TCCTTGTCCT	TGTTTTAAAA	GGTGTCCAGT
	AGTGGTACTT	GAAGCCCAAG	TCGAACTAAA	AGGAACAGGA	ACAAAATTTT	CCACAGGTCA
61	GTGAAGTGGT	GGTGGTGGAG	TCTGGGGGAG	GCTTCGTGAA	GCCTGGAGGG	TCCCTGAAAC
	CACTTCACCA	CCACCACCTC	AGACCCCCTC	CGAAGCACTT	CGGACCTCCC	AGGGACTTTG
121	TCTCCTGTGC	AGCCGCTGGA	TTCACTTTCA	GTAGATATGC	CATGTCTTGG	GTTCGCCAGA
	AGAGGACACG	TCGGCGACCT	AAGTGAAAGT	CATCTATACG	GTACAGAACC	CAAGCGGTCT
181	CTCCGGAGAA	GAGGCTGGAG	TGGGTCGCAA	CCATAAGTAG	TGGTGGTAGT	CACACCTACT
	GAGGCCTCTT	CTCCGACCTC	ACCCAGCGTT	GGTATTCATC	ACCACCATCA	GTGTGGATGA
241	ATCCAGACAG	TGTGAAGGGG	CGATTCACCA	TCTCCAGAGA	CAATGCCAAG	AACACCCTGT
i i i miq	TAGGTCTGTC	ACACTTCCCC	GCTAAGTGGT	AGAGGTCTCT	GTTACGGTTC	TTGTGGGACA
301	ACCTGCAAAT	GAGCAGTCTG	AGGTCTGAGG	ACACGGCCAT	ATATTACTGT	GCAAGACCGG
	TGGACGTTTA	CTCGTCAGAC	TCCAGACTCC	TGTGCCGGTA	TATAATGACA	CGTTCTGGCC
361	GTTACGACAG	GGGGGCCTGG	TTTTTCGATG	TCTGGGGCGC	AGGGACCACG	GTCACCGTCT
	CAATGCTGTC	CCCCCGGACC	AAAAAGCTAC	AGACCCCGCG	TCCCTGGTGC	CAGTGGCAGA
421	CCTCAGGTAA	GTGTGTCAGG	GTTTCACAAG	AGGGACTAAA	GACATGTCAG	CTAATGTGTG
\$7.5 #	GGAGTCCATT	CACACAGTCC	CAAAGTGTTC	TCCCTGATTT	CTGTACAGTC	GATTACACAC
481	ACTAATGGTA	ATGTCACTAA	GCTT			
IAJ	TGATTACCAT	TACAGTGATT	CGAA			

Fig. 4A Juralians NAME: BMB3.6-L-Ch 483 BPS DNA UPDATED 6/25/93

DESCRIPTION: light chain leader and variable region of bmb3.6 C

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* * * SEQUENCE * * *

	1					GACTTATGCT	
		TCCCTTTCGA	GCTTCTACCA	AAAGTGTGGA	GTCTATGAAC	CTGAATACGA	AAAAACCTAA
	61	TCAGCCTCCA	GAGGTGATAT	TGTGCTAACT	CAGTCTCCAG	CCACCCTGTC	TGTGACTCCA
		AGTCGGAGGT	CTCCACTATA	ACACGATTGA	GTCAGAGGTC	GGTGGGACAG	ACACTGAGGT
	121	GGAGATAGCG	TCAGTCTTTC	CTGCAGGGCC	AGCCAAATTA	TTAGCAACAA	CCTACACTGG
		CCTCTATCGC	AGTCAGAAAG	GACGTCCCGG	TCGGTTTAAT	AATCGTTGTT	GGATGTGACC
	181	TATCAACAAA	AATCACATGA	GTCTCCAAGG	CTTCTCATCA	AGTATGCTTC	CCAGTCCATC
	-	ATAGTTGTTT	TTAGTGTACT	CAGAGGTTCC	GAAGAGTAGT	TCATACGAAG	GGTCAGGTAG
	241	TCTGGGATCC	CCTCCAGGTT	CAGTGGCAGT	GGATCAGGGA	CAGATTTCAC	TCTCAGTATC
ļ.		AGACCCTAGG	GGAGGTCCAA	GTCACCGTCA	CCTAGTCCCT	GTCTAAAGTG	AGAGTCATAG
	301	AACAGTGTGG	AGACTGAAGA	TTTTGGAATG	TATTTCTGTC	AACAGAGTAA	CAGCTGGCCT
16		TTGTCACACC	TCTGACTTCT	AAAACCTTAC	ATAAAGACAG	TTGTCTCATT	GTCGACCGGA
TE1	361	CTCACGTTCG	GCTCGGGGAC	AAAGCTGGAG	ATCAAACGGC	GTAAGTGTGT	CAGGGTTTCA
		GAGTGCAAGC	CGAGCCCCTG	TTTCGACCTC	TAGTTTGCCG	CATTCACACA	GTCCCAAAGT
	421	CAAGAGGGAC	TAAAGACATG	TCAGCTAATG	TGTGACTAAT	GGTAATGTCA	CTTGTCAGGA
		GTTCTCCCTG	ATTTCTGTAC	AGTCGATTAC	ACACTGATTA	CCATTACAGT	GAACAGTCCT
[ash	481	TCC					
74,		AGG					

Fig. 4B Longhans

NAME: sFv MB3.6

The tells

DESCRIPTION: Light chain leader plus sFv of MB3.6

* * * SEQUENCE * * *

+vector Xb2I Start -- leader 1 GATATCAGAT CTCAGCTGTC TAGACATATG GTTTTCACAC CTCAGATANN NNNNNNNNN OPF D I R S Q L S R H M V F T P Q I I S D L S C L D I W F S H L R ? YQISAV-TYGFHTSD???? leader + T + VL ? ? ? ? ? ? ? ? ? ? ? ? ? ? G Q S W ? ? ? ? ? ? ? ? ? P K A G Linker 47 > VH VL4-+Linker ATCAAAGGTG GCTCAGGATC GGGTGGAGCC GGCTCTGGTG GCTCAGGATC GGAAGTGGTG RSKVAQDRVEPALV A Q D D Q R W L R I G W S R L W Z VH 4 →TCR E/h3 ACGGTCACCG TCTCCAGT T V T V S S P R S P S P 1 L HGH RLQ 票

> Fig.4C Lunghans

FILE NAME : 3D8HCDNA.SEQ

SEQUENCE: 682BP; 153 A; 184 C; 173 G; 172 T.

*** SEQUENCE LIST ***

(DOUBLE)

-,	10	20	30	40	50	60
5'		CCCCTCACCA	TGAACTTCGG	GCTCAGCTTG	ATTTTCCTTG	TCCTTGTTTT
3′		GGGGAGTGGT		CGAGTCGAAC	TAAAAGGAAC	AGGAACAAAA
	70	80	90	100	110	120
	AAAAGGTGTC	CAGTGTGAAG	TGAAGGTGGT	GGAGTCTGGG	GGAGGCTTAG	TGAAGCCTGG
		GTCACACTTC		CCTCAGACCC	CCTCCGAATC	ACTTCGGACC
_	130	140	150	160	170	180
1-1		AAACTCTCCT				
4.1	TCGCAGAGAC		CACGTCGGAG	ACCTAAGTGA	AAGTCATTGA	TACCGTACAG
f#1	190	200	210	220	230	240
	TTGGGTTCGC	CAGACTTCAG	ACAAGAGGCT	GGAGTGGGTC	GCATCCATTA	GTAGTGGTGG
ar i		GTCTGAAGTC	TGTTCTCCGA	CCTCACCCAG	CGTAGGTAAT	CATCACCACC
'n,į	250	260	270	280	290	300
Tar Tari	TGATAGCACC	TTCTATGCAG	ACAATGTAAA	GGGCCGATTC	ACCATCTCCA	GAGAGAATGC
# 1		AAGATACGTC	TGTTACATTT	CCCGGCTAAG	TGGTAGAGGT	CTCTCTTACG
	310	320	330	340	350	360
# }-1	CAAGAACACC	CTGTACCTGC	AAATGAGTAG	TCTGAAGTCT	GAGGACACGG	CCTTGTATTA
21444 1916 B		GACATGGACG	TTTACTCATC	AGACTTCAGA	CTCCTGTGCC	GGAACATAAT
	370	380	390	400	410	420
jina	CTGTGCAAGA	GACGATCTAT	TTAACTGGGG	CCAAGGCACC	ACTCTCACAG	TCTCATCAGC
		CTGCTAGATA	AATTGACCCC	GGTTCCGTGG	TGAGAGTGTC	AGAGTAGTCG
	430	440	450	460	470	480
ļļak	CAAAACAACA	GCCCCATCGG	TCTATCCACT	GGCCCCTGTG	TGTGGAGATA	CAATTGGCTC
	GTTTTGTTGT	CGGGGTAGCC	AGATAGGTGA	CCGGGGACAC	ACACCTCTAT	GTTAACCGAG
	490	500	510	520	530	540
	CTCGGTGACT	TTAGGATGCC	TGGTCAAGGG	TTATTTCCTT	GAGCCAGTGA	CCTTGACCTG
	GAGCCACTGA	AATCCTACGG	ACCAGTTCCC	AATAAAGGAA	CTCGGTCACT	GGAACTGGAC
	550	560	570	580	590	600
	GAACTCTGGA	TCCCTGTCCA	GTGGTGTGCA	CATCTTCCCA	GCTGTCTTGC	AGTCTGACCT
	CTTGAGACCT	AGGGACAGGT	CACCACACGT	GTAGAAGGGT	CGACAGAACG	TCAGACTGGA
	610	620	630	640	650	660
	CTACACCCTC	AGCAGCTCAG	TGACTGTAAC	CTCGAGCACC	TGGCCCAGCC	AGTCCATCAC
	GATGTGGGAG	TCGTCGAGTC	ACTGACATTG	GAGCTCGTGG	ACCGGGTCGG	TCAGGTAGTG
	670	680				
	TTGCAATGTG	GCCCACCCGG	CA 3'			
	AACGTTACAC	CGGGTGGGCC	GT 5'			

FILE NAME : 3D8LCDNA.SEQ

SEQUENCE: 729BP; 203 A; 177 C; 172 G; 177 T.

*** SEQUENCE LIST *** (DOUBLE)

	10	20	30	40	50	60
57				TCCTGTTTCT		• • • • • • • • • • • • • • • • • • • •
31				AGGACAAAGA		
3	70	80	90	100	110	120
	AAACCAACGG			CTCCACTCAC		ACCATTGGAC
	TTTGGTTGCC	ACTACAACAT		GAGGTGAGTG		
	130	140	150	160	170	180
		TATCTCTTGC	AAGTCAAGTC	AGAGCCTCTT	ATATAGTAAT	GGAAAAACCT
	TTGGTCGGAG	ATAGAGAACG	TTCAGTTCAG	TCTCGGAGAA	TATATCATTA	CCTTTTTGGA
	190	200	210	220	230	240
#= 	ATTTGAATTG	GTTATTACAG	AGGCCAGGCC	AGTCTCCAAA	GCGCCTAATC	TATCTGGTGT
47	TAAACTTAAC	CAATAATGTC	TCCGGTCCGG	TCAGAGGTTT	CGCGGATTAG	ATAGACCACA
Ant l	250	260	270	280	290	300
	CTAAACTGGA	CTCTGGAGTC	CCTGACAGGT	TCACTGGCAG	TGGATCAGGA	ACAGATTTTA
	GATTTGACCT	GAGACCTCAG	GGACTGTCCA	AGTGACCGTC	ACCTAGTCCT	TGTCTAAAAT
4,1	310	320	330	340	350	360
, i	CACTGAAAAT			ATTTGGGAGT		
- [[]	GTGACTTTTA	GTCGTCTCAC	CTCCGACTCC	TAAACCCTCA	AATAATGACG	CACGTTCCAT
18	370	380	390	400	410	420
ila.				CCAAGCTGGA		
				GGTTCGACCT		
ill	430	440	450	460	470	480
				GTGAGCAGTT		
THE STATE OF	GTGGTTGACA			CACTCGTCAA		
ilan# ii i	490	500	510	520	530	540
(H=18	TCGTGTGCTT			AAGACATCAA		
				TTCTGTAGTT		
	550	560	570	580	590	600
				GTTGGACTGA		
	CGTCACTTGC	TGTTTTACCG				TTTCTGTCGT
	610	620	630	640	650	660
	CCTACAGCAT	GAGCAGCACC		CCAAGGACGA		
	GGATGTCGTA			GGTTCCTGCT	CATACTTGCT	GTATTGTCGA
	670	088	690	700	710	720
	ATACCTGTGA			CTTCACCCAT	TGTCAAGAGC	TTCAACAGGA
	TATGGACACT	CCGGTGAGTG	TTCTGTAGTT	GAAGTGGGTA	ACAGTTCTCG	AAGTTGTCCT

ATGAGTGTT 3'

TACTCACAA 5'

FILE NAME: 4D4HCDNA.SEQ

SEQUENCE: 736BP; 170 A; 210 C; 186 G; 170 T.

*** SEQUENCE LIST *** (DOUBLE)

20 30 40 5' ACTGACTCTA ACCATGGGAT GGAGATGGAT CTTTCTTTTC CTCCTGTCAG GAACTGCAGG 3' TGACTGAGAT TGGTACCCTA CCTCTACCTA GAAAGAAAAG GAGGACAGTC CTTGACGTCC 80 90 100 TGTCCATTGC CAGGTTCAGC TGCAGCAGTC TGGACCTGAG CTGGTGAAGC CTGGGGCTTT ACAGGTAACG GTCCAAGTCG ACGTCGTCAG ACCTGGACTC GACCACTTCG GACCCCGAAA 140 150 160 AGTGAAGATA TCCTGCAAGG CTTCTGGTTA CACCTTCACA AGCTACGATA TAAACTGGGT TCACTTCTAT AGGACGTTCC GAAGACCAAT GTGGAAGTGT TCGATGCTAT ATTTGACCCA 200 210 220 GAAGCAGAGG CCTGGACAGG GACTTGAGTG GATTGGATGG ATTTATCCTG GAGATGGTGG CTTCGTCTCC GGACCTGTCC CTGAACTCAC CTAACCTACC TAAATAGGAC CTCTACCACC 260 270 280 TACTAATTAC AATGAGAAAT TCAAGGGCAA GGCCACACTG ACTGCAGACA AATCCTCCAG ATGATTAATG TTACTCTTTA AGTTCCCGTT CCGGTGTGAC TGACGTCTGT TTAGGAGGTC 320 330 340 * CACAGCCTAC ATGCAGCTCA GTAGCCTGAC TTCTGAGAAC TCTGCAGTCT ATTTCTGTGC FIGTCGGATG TACGTCGAGT CATCGGACTG AAGACTCTTG AGACGTCAGA TAAAGACACG 390 400 👫 AAGAGGGGGT AACTTCCCTT CTTATGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC TTCTCCCCCA TTGAAGGGAA GAATACGATA CCTGATGACC CCAGTTCCTT GGAGTCAGTG 440 450 460 470 CGTCTCCTCA GCCAAAACGA CACCCCCATC TGTCTATCCA CTGGCCCCTG GATCTGCTGC GCAGAGGAGT CGGTTTTGCT GTGGGGGTAG ACAGATAGGT GACCGGGGAC CTAGACGACG 490 500 510 520 CCAAACTAAC TCCATGGTGA CCCCGGGATG CCTGGTCAAG GGCTATTTCC CTGAGCCAGT GGTTTGATTG AGGTACCACT GGGGCCCTAC GGACCAGTTC CCGATAAAGG GACTCGGTCA 560 570 580 GACAGTGACC TGGAACTCTG GATCCCTGTC CAGCGGTGTG CACACCTTCC CAGCTGTCCT CTGTCACTGG ACCTTGAGAC CTAGGGACAG GTCGCCACAC GTGTGGAAGG GTCGACAGGA 630 640 620 GCAGTCTGAC CTCTACACTC TGAGCAGCTC AGTGACTGTC CCCTCCAGCA CCTGGCCCAG CGTCAGACTG GAGATGTGAG ACTCGTCGAG TCACTGACAG GGGAGGTCGT GGACCGGGTC 680 690 700 CGAGACCGTC ACCTGCAACG TTGCCCACCC GGCCAGCAGC ACCAAGGTGG ACAAGAAAAT GCTCTGGCAG TGGACGTTGC AACGGGTGGG CCGGTCGTCG TGGTTCCACC TGTTCTTTTA TGTGCCCAGG GATTGT 3' ACACGGGTCC CTAACA 5'

FILE NAME: 4D4LCDNA.SEQ

SEQUENCE: 504BP; 120 A; 126 C; 122 G; 136 T.

(DOUBLE) *** SEQUENCE LIST ***

AAGAACTTGT TGAAGATGGG GTTT 5'

	10	20	30	40	50	60
5 <i>'</i>	CTCAAAATGA			GTGCTGATGT		
3 <i>'</i>	GAGTTTTACT	TCAACGGACA	ATCCGACAAC	CACGACTACA	AGACCTAAGG	ACGAAGGTTG
	70	80	90	100	110	120
	AGTGATGTTT	TGATGACCCA	ATCTCCACTC	TCCCTGCCTG	TCAGTCTTGG	AGATCAAGCC
	TCACTACAAA	ACTACTGGGT	TAGAGGTGAG	AGGGACGGAC	AGTCAGAACC	TCTAGTTCGG
	130	140	150	160	170	180
en i	TCCATCTCTT	GCAGATCTAG	TCAGAGCATT	GTCCATAGTA	ATGGAGACAC	CTATTTAGAA
	AGGTAGAGAA	CGTCTAGATC	AGTCTCGTAA	CAGGTATCAT	TACCTCTGTG	GATAAATCTT
#*1	190	200	210	220	230	240
45	TGGTACCTGC	AGAAACCAGG	CCAGTCTCCA	AAGCTCCTGA	TCTACAAGGT	TTCCGACCGA
res res	ACCATGGACG	TCTTTGGTCC	GGTCAGAGGT	TTCGAGGACT	AGATGTTCCA	AAGGCTGGCT
April April	250	260	270	280	290	300
41	TTTTCTGGGG	TCCCAGACAG	GTTCAGTGGC	AGTGGATCAG	GGACAGATTT	CACACTCAAG
144	AAAAGACCCC	AGGGTCTGTC	CAAGTCACCG	TCACCTAGTC	CCTGTCTAAA	GTGTGAGTTC
44.	310	320	330	340	350	360
#				GTTTATTTCT		
ija k	TAGTCGTCTC	ACCTCCGACT	CCTAGACCCT	CAAATAAAGA	CGAAAGTTCC	AAGTGTACAA
T.	370	380	390	400	410	420
p.	CCGTACGCGT	TCGGAGGGG	GACCAAGCTG	GAAATAAAAC	GGGCTGATGC	TGCACCAACT
	GGCATGCGCA	AGCCTCCCCC	CTGGTTCGAC	CTTTATTTTG	CCCGACTACG	ACGTGGTTGA
ani.	430	440	450	460	470	480
-	GTATCCATCT	TCCCACCATC	CAGTGAGCAG	TTAACATCTG	GAGGTGCCTC	AGTCGTGTGC
	CATAGGTAGA	AGGGTGGTAG	GTCACTCGTC	AATTGTAGAC	CTCCACGGAG	TCAGCACACG
	490	500				
	TTCTTGAACA	ACTTCTACCC	CAAA 3'			

FILE NAME : 3E11HCDN.SEQ

SEQUENCE: 761BP; 167 A; 213 C; 188 G; 193 T.

*** SEQUENCE LIST *** (DOUBLE)

	10	20	20	4.0	5.0	
5′	10	20 ATTTCCAGTT	30	40	50	60
31		TAAAGGTCAA				
J .	70	80	90			
				100	110	120
		GGGCTCAGCT				
	130	CCCGAGTCGA				
ļui		140	150	160	170	180
77		GTGGAGTCTG				
		CACCTCAGAC				
	190	200	210	220	230	240
775		TCTGGATTCA				
		AGACCTAAGT				
74	250	260	270	280	290	300
7-1		CTGGAGTGGG				
		GACCTCACCC				
Œ	310	320	330	340	350	360
in.		AAGGGCCGAT				
FLI		TTCCCGGCTA				
ļa!	370	380	390	400	410	420
		AGTCTGAAGT				
		TCAGACTTCA				
	430	440	450	460	470	480
p==		TGTTGGTTTG				
		ACAACCAAAC				
	490	500	510	520	530	540
	CAAAACAACA	CCCCCATCAG	TCTATCCACT	GGCCCCTGGG	TGTGGAGATA	CTĄCTGGTTC
		GGGGGTAGTC				
	550	560	570	580	590	600
		CTGGGATGCC				
		GACCCTACGG				
	610	620	630	640	650	660
		TCCCTGCCCA				
		AGGGACGGGT				TCAGACCTGA
	670	680	690	700	710	720
		AGCAGCTCAG				
	GATGTGATAC			GAGGTCGTGG	ACCGGTTCGG	TCTGGCAATG
	730	740	750	760		
		GCTCACCCAG				
	GACGTCACAA	CGAGTGGGTC	GGTCGTCGTG	GTGCCACCTG	T 5'	

FILE NAME : 3E11LCDN.SEQ

SEQUENCE: 698BP; 199 A; 179 C; 167 G; 153 T.

*** SEQUENCE LIST ***

(DOUBLE)

	10	20	30	40	50	60
5 ′		CATCAAGATG				
3 ′	GGTCGTACCC	GTAGTTCTAC	CTTAGTGTCT	GAGACCAGAA	GTATAGGTAT	GACGAGACCA
	70	80	90	100	110	120
		TGATGGGAAC				
		ACTACCCTTG	TAACATTACT	GGGTTAGAGG	GTTTAGGTAC	AGGTACAGTC
. jania	130	140	150	160	170	180
		GGTCACCTTG				
######################################		CCAGTGGAAC	TGGACGTTCC	GGTCACTCTT	ACACCAATGA	ATACAAAGGA
747 747	190	200	210	220	230	240
And and		GAAACCAGAG				
71	CCATAGTTGT	CTTTGGTCTC	GTCAGAGGAT	TTGACGACTA	TATGCCCCGT	AGGTTGGCCA
A firm	250	260	270	280	290	300
4.1	ACACTGGGGT	CCCCGATCGC	TTCACAGGCA	GTGGATCTGC	AACAGATTTC	ACTCTGACCA
		GGGGCTAGCG			TTGTCTAAAG	TGAGACTGGT
18	310	320	330	340	350	360
jania 1	TCAGCAGTGT	GCAGGCTGAA	GACCTTGCAG	ATTATCACTG	TGGACAGGGT	TACAGCTATC
Full.		CGTCCGACTT				ATGTCGATAG
ļļ-4	370	380	390	400	410	420
	CGTACACGTT	CGGAGGGGG	ACCAAGCTGG	AAATAAAACG	GGCTGATGCT	GCACCAACTG
		GCCTCCCCC				
in.	430	440	450	460	470	480
7	TATCCATCTT	CCCACCATCC	AGTGAGCAGT	TAACATCTGG	AGGTGCCTCA	GTCGTGTGCT
		GGGTGGTAGG				CAGCACACGA
	490	. 500	510	520	530	540
	TCTTGAACAA	CTTCTACCCC	AAAGACATCA	ATGTCAAGTG	GAAGATTGAT	GGCAGTGAAC
		GAAGATGGGG				
	550	560	570	580	590	600
		CGTCCTGAAC				
		GCAGGACTTG		TAGTCCTGTC		
	610	620	630	640	650	660
	TGAGCAGCAC	CCTCACGTTG	ACCAAGGACG	AGTATGAACG	ACATAACAGC	TATACCTGTG
		GGAGTGCAAC		TCATACTTGC	TGTATTGTCG	ATATGGACAC
	670	680	690	maama:		
		CAAGACATCA				
	TCCGGTGAGT	GTTCTGTAGT	TGAAGTGGGT	AGCAGTTC 5	•	

Fig. 4I Junghans

Anti-Melanoma IgTCR Tumor Targeting

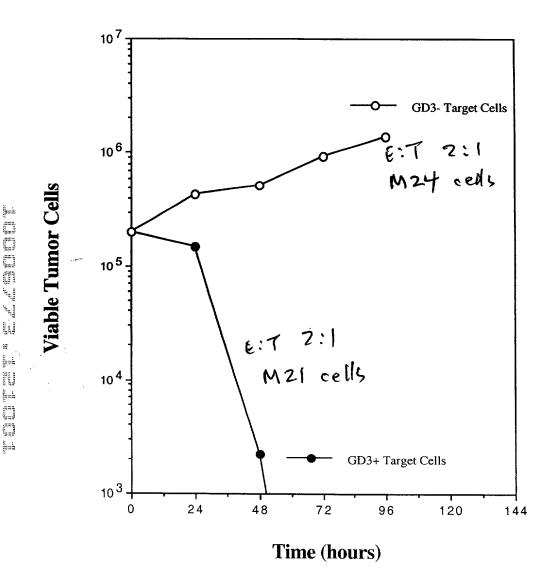


Fig. 5 Junghans

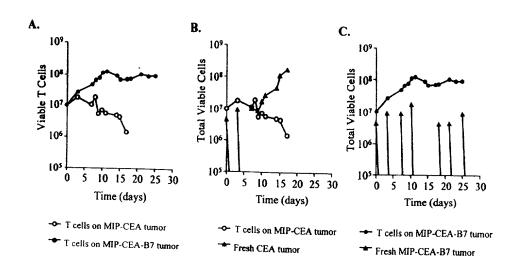
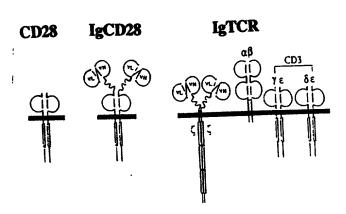


Fig. 6 Junghans



Fisi7 Junghans